

Amendments to the Claims:

The following Listing of Claims will replace all prior versions, and listings, of the claims in the above-identified application.

Listing of Claims

1. (currently amended) An isolated and purified-poly(ADP-ribose) polymerase (PARP) homolog comprising human PARP2 (SEQ ID NO: 2) or a functional equivalent thereof which is at least 85% homologous thereto, exhibits poly(ADP-ribose)-synthesizing activity, and has an amino acid sequence which
 - a) has a functional NAD^+ binding domain comprising the sequence motif $\text{PX}_n(\text{S/T})\text{GX}_3\text{GKGIYFA}$ (SEQ ID NO:11) in which n is an integral value from 1 to 5, and the X radicals are, independently of one another, any amino acid;and
 - b) lacks a zinc finger sequence motif of the ~~general~~ formula $\text{CX}_2\text{CX}_m\text{HX}_2\text{C}$ (SEQ ID NO:30) in which m is an integral value of 28 or 30, and the X radicals are, independently of one another, any amino acid.
2. (currently amended) The PARP homolog as claimed in claim 1, wherein the functional NAD^+ binding domain comprises ~~one of~~ the following ~~general~~ sequence motifs:
 $(\text{S/T})\text{XGLR}(\text{I/V})\text{XPX}_n(\text{S/T})\text{GX}_3\text{GKGIYFA}$ (SEQ ID NO:12) or
 $\text{LLWHG}(\text{S/T})\text{X}_2\text{IL}(\text{S/T})\text{XGLR}(\text{I/V})\text{XPX}_n(\text{S/T})\text{GX}_3\text{GKGIYFAX}_3\text{SKSAXY}$ (SEQ ID NO:13)
in which n is an integral value from 1 to 5, and the X radicals are, independently of one another, any amino acid.

3. (currently amended) The PARP homolog as claimed in claim 1, further comprising at least another one of the following part-sequence motifs:

LX₉NX₂YX₂QLLX(D/E)X_{10/11}WGRVG (SEQ ID NO: 15);

~~AX₃FXXKX₄KTXNXWX₅FX₃PXK (SEQ ID NO:16);~~

QXL(I/L)X₂IX₉MX₁₀PLGKLX₃QIX₆L (SEQ ID NO:17);

FYTXIPHXFGX₃PP (SEQ ID NO:18); and

KX₃LX₂LXDIEXAX₃L (SEQ ID NO:19);

in which the X radicals are, independently of one another, any amino acid.

- 4-32. (canceled)

33. (new) The PARP homolog as claimed in claim 1, wherein the functional NAD⁺ binding domain comprises the following sequence motif:

LLWHG(S/T)X₇IL(S/T)XGLR(I/V)XPX_n(S/T)GX₃GKGIYFAX₃SKSAXY (SEQ ID NO:13)

in which n is an integral value from 1 to 5, and

the X radicals are, independently of one another, any amino acid.

34. (new) The PARP homolog as claimed in claim 1 further comprising part-sequence motif

AX₃FXXKX₄KTXNXWX₅FX₃PXK (SEQ ID NO:16)

in which the X radicals are, independently of one another, any amino acid.

35. (new) The PARP homolog as claimed in claim 1 further comprising part-sequence motif

XL(I/L)X₂IX₉MX₁₀PLGKLX₃QIX₆L (SEQ ID NO:17)

in which the X radicals are, independently of one another, any amino acid.

36. (new) The PARP homolog as claimed in claim 1 further comprising part-sequence motif

FYTXIPHXFGX₃PP (SEQ ID NO:18)

in which the X radicals are, independently of one another, any amino acid.

37. (new) The PARP homolog as claimed in claim 1 further comprising part-sequence motif
KX₃LX₂LXDIEXAX₂L (SEQ ID NO:19)

in which the X radicals are, independently of one another, any amino acid.

38. (new) An isolated poly(ADP-ribose) polymerase (PARP) homolog comprising human PARP2 (SEQ ID NO: 2) or a functional equivalent thereof which is at least 85% homologous thereto, exhibits poly(ADP-ribose)-synthesizing activity, and has an amino acid sequence which

- a) has a functional NAD⁺ binding domain comprising the sequence motif
PX_n(S/T)GX₃GKGIYFA (SEQ ID NO:11)

in which n is an integral value from 1 to 5, and the X radicals are, independently of one another, any amino acid;

and

- b) lacks a zinc finger sequence motif of the formula
CX₂CX_mHX₂C (SEQ ID NO:30)

in which m is an integral value of 28 or 30, and the X radicals are, independently of one another, any amino acid

further comprising a leucine zipper-like sequence motif:

(L/V)X₆LX₆LX₆L (SEQ ID NO: 14)

wherein X radicals are, independently of one another, any amino acid.

39. (new) The PARP homolog as claimed in claim 38 further comprising at least one of the following part-sequence motifs:

LX₉NX₂YX₂QLX(D/E)X_{10/11}WGRVG (SEQ ID NO: 15),

AX₃FXXKX₄KTXNXWX₅FX₃PXK (SEQ ID NO:16),

QXL(I/L)X₂IX₉MX₁₀PLGKLX₃QIX₆L (SEQ ID NO:17),

FYTXIPHXFGX₃PP (SEQ ID NO:18), and

KX₃LX₂LXDIEXAX₂L (SEQ ID NO:19)

in which the X radicals are, independently of one another, any amino acid.

40. (new) The PARP homolog as claimed in claim 38 further comprising part-sequence motifs:

LX₉NX₂YX₂QLLX(D/E)X_{10/11}WGRVG (SEQ ID NO: 15)

AX₃FXXKX₄KTXNXWX₅FX₃PXK (SEQ ID NO:16),

QXL(I/L)X₂IX₉MX₁₀PLGKLX₃QIX₆L (SEQ ID NO:17),

FYTXIPHXFGX₃PP (SEQ ID NO:18), and

KX₃LX₂LXDIEXAX₂L (SEQ ID NO:19)

in which the X radicals are, independently of one another, any amino acid.

41. (new) The PARP homolog as claimed in claim 38 further comprising part-sequence motifs:

LX₉NX₂YX₂QLLX(D/E)X_{10/11}WGRVG (SEQ ID NO: 15)

AX₃FXXKX₄KTXNXWX₅FX₃PXK (SEQ ID NO:16),

QXL(I/L)X₂IX₉MX₁₀PLGKLX₃QIX₆L (SEQ ID NO:17),

FYTXIPHXFGX₃PP (SEQ ID NO:18), and

KX₃LX₂LXDIEXAX₂L (SEQ ID NO:19)

in which the X radicals are, independently of one another, any amino acid, wherein

LX₉NX₂YX₂QLLX(D/E)X_{10/11}WGRVG (SEQ ID NO:15)

is closest to the N terminus.

42. (new) The PARP homolog as claimed in claim 1 further comprising part-sequence motifs:

LX₉NX₂YX₂QLLX(D/E)X_{10/11}WGRVG (SEQ ID NO: 15)

AX₃FXXKX₄KTXNXWX₅FX₃PXK (SEQ ID NO:16),

QXL(I/L)X₂IX₉MX₁₀PLGKLX₃QIX₆L (SEQ ID NO:17),

FYTXIPHXFGX₃PP (SEQ ID NO:18), and

KX₃LX₂LXDIEXAX₂L (SEQ ID NO:19)

in which the X radicals are, independently of one another, any amino acid.

43. (new) The PARP homolog as claimed in claim 1 further comprising part-sequence motifs:

LX₉NX₂YX₂QLLX(D/E)X_{10/11}WGRVG (SEQ ID NO: 15)

AX₃FXX₄KTXNXWX₅FX₃PXK (SEQ ID NO:16),

QXL(I/L)X₂IX₉MX₁₀PLGKLX₃QIX₆L (SEQ ID NO:17),

FYTXIPHXFGX₃PP (SEQ ID NO:18), and

KX₃LX₂LXDIEXAX₂L (SEQ ID NO:19)

in which the X radicals are, independently of one another, any amino acid, wherein

LX₉NX₂YX₂QLLX(D/E)X_{10/11}WGRVG (SEQ ID NO:15)

is closest to the N terminus.

44. (new) The PARP homolog as claimed in claim 1 further comprising at least one of the following:

GX₃LXVALG (SEQ ID NO: 20),

GX₂SX₄GX₃PX_aLXGX₂V (SEQ ID NO: 21), and

E(Y/F)X₂YXYX₃QXYLL (SEQ ID NO: 22)

in which a is 7 to 9 and

X is any amino acid.

45. (new) The PARP homolog as claimed in claim 1 further comprising

GX₃LXEVALG (SEQ ID NO: 20),

GX₂SX₄GX₃PX_aLXGX₂V (SEQ ID NO: 21), and

E(Y/F)X₂YX₃QX_aYLL (SEQ ID NO: 22)

in which a is 7 to 9 and

X is any amino acid.

46. (new) The PARP homolog as claimed in claim 1 further comprising

GX₃LXEVALG (SEQ ID NO: 20),

GX₂SX₄GX₃PX_aLXGX₂V (SEQ ID NO: 21), and

E(Y/F)X₂YX₃QX₄YLL (SEQ ID NO: 22)

in which a is 7 to 9 and

X is any amino acid, wherein

E(Y/F)X₂YX₃QX₄YLL (SEQ ID NO: 22)

is closest to the C terminus.

47. (new) An isolated poly(ADP-ribose) polymerase (PARP) homolog comprising human PARP2 (SEQ ID NO: 2) or a functional equivalent thereof which is at least 85% homologous thereto, exhibits poly(ADP-ribose)-synthesizing activity, and has an amino acid sequence which

- a) has a functional NAD⁺ binding domain comprising the sequence motif

PX_n(S/T)GX₃GKGIYFA (SEQ ID NO:11)

in which n is an integral value from 1 to 5, and the X radicals are, independently of one another, any amino acid;

and

- b) lacks a zinc finger sequence.

48. (new) The PARP homolog as claimed in claim 47 wherein said PARP lacks a zinc finger sequence motif of the formula

CX₂CX_mHX₂C (SEQ ID NO:30)

in which m is an integral value of 28 or 30, and

the X radicals are, independently of one another, any amino acid.

49. (new) The PARP homolog as claimed in claim 47 wherein the functional NAD⁺ binding domain comprises the following sequence motif:

(S/T)XGLR(I/V)XPX_n(S/T)GX₃GKGIYFA (SEQ ID NO:12)

in which n is an integral value from 1 to 5, and

the X radicals are, independently of one another, any amino acid.

50. (new) The PARP homolog as claimed in claim 47 wherein the functional NAD⁺ binding domain comprises the following sequence motif:

LLWHG(S/T)X₇IL(S/T)XGLR(I/V)XPX_n(S/T)GX₃GKGIYFAX₃SKSAXY (SEQ ID NO:13)

in which n is an integral value from 1 to 5, and

the X radicals are, independently of one another, any amino acid.

51. (new) The PARP homolog as claimed in claim 47 further comprising a leucine zipper-like sequence:

(L/V)X₆LX₆LX₆L (SEQ ID NO: 14)

wherein X radicals are, independently of one another, any amino acid.

52. (new) The PARP homolog as claimed in claim 51 further comprising at least one of the following part-sequence motifs:

LX₉NX₂YX₂QLLX(D/E)X_{10/11}WGRVG (SEQ ID NO: 15),

AX₃FXKX₄KTXNXWX₅FX₃PXK (SEQ ID NO:16),

QXL(I/L)X₂IX₉MX₁₀PLGKLX₃QIX₆L (SEQ ID NO:17),

FYTXIPHFXGX₃PP (SEQ ID NO:18), and

KX₃LX₂LXDIEXAX₂L (SEQ ID NO:19)

in which the X radicals are, independently of one another, any amino acid.

53. (new) The PARP homolog as claimed in claim 51 further comprising:

LX₉NX₂YX₂QLLX(D/E)X_{10/11}WGRVG (SEQ ID NO: 15),
AX₃FXKX₄KTXNXWX₅FX₃PXK (SEQ ID NO:16),
QXL(I/L)X₂IX₉MX₁₀PLGKLX₃QIX₆L (SEQ ID NO:17),
FYTXIPHXFGX₃PP (SEQ ID NO:18), and
KX₃LX₂LXDIEXAX₂L (SEQ ID NO:19)

in which the X radicals are, independently of one another, any amino acid.

54. (new) The PARP homolog as claimed in claim 51 further comprising:

LX₉NX₂YX₂QLLX(D/E)X_{10/11}WGRVG (SEQ ID NO: 15),
AX₃FXKX₄KTXNXWX₅FX₃PXK (SEQ ID NO:16),
QXL(I/L)X₂IX₉MX₁₀PLGKLX₃QIX₆L (SEQ ID NO:17),
FYTXIPHXFGX₃PP (SEQ ID NO:18), and
KX₃LX₂LXDIEXAX₂L (SEQ ID NO:19)

in which the X radicals are, independently of one another, any amino acid, wherein

LX₉NX₂YX₂QLLX(D/E)X_{10/11}WGRVG (SEQ ID NO: 15)

is closest to the N terminus.

55. (new) The PARP homolog as claimed in claim 47 further comprising at least one of the following:

GX₃LXEVALG (SEQ ID NO: 20),
GX₂SX₄GX₃PX_aLXGX₂V (SEQ ID NO: 21), and
E(Y/F)X₂YX₃QX₄YLL (SEQ ID NO: 22)

in which a is 7 to 9 and

X is any amino acid.

56. (new) The PARP homolog as claimed in claim 47 further comprising

GX₃LXEVALG (SEQ ID NO: 20),

GX₂SX₄GX₃PX_aLXGX₂V (SEQ ID NO: 21), and

E(Y/F)X₂YX₃QX₄YLL (SEQ ID NO: 22)

in which a is 7 to 9 and

X is any amino acid.

57. (new) The PARP homolog as claimed in claim 47 further comprising

GX₃LXEVALG (SEQ ID NO: 20),

GX₂SX₄GX₃PX_aLXGX₂V (SEQ ID NO: 21), and

E(Y/F)X₂YX₃QX₄YLL (SEQ ID NO: 22)

in which a is 7 to 9 and

X is any amino acid, wherein

E(Y/F)X₂YX₃QX₄YLL (SEQ ID NO: 22)

is closest to the C terminus.

58. (new) The PARP homolog as claimed in claim 51 further comprising at least one of the following:

GX₃LXVALG (SEQ ID NO: 20),

GX₂SX₄GX₃PX_aLXGX₂V (SEQ ID NO: 21), and

E(Y/F)X₂YX₃QX₄YLL (SEQ ID NO: 22)

in which a is 7 to 9 and

X is any amino acid.

59. (new) The PARP homolog as claimed in claim 51 further comprising

GX₃LXEVALG (SEQ ID NO: 20),

GX₂SX₄GX₃PX_aLXGX₂V (SEQ ID NO: 21), and

E(Y/F)X₂YX₃QX₄YLL (SEQ ID NO: 22)

in which a is 7 to 9 and

X is any amino acid.

60. (new) The PARP homolog as claimed in claim 51 further comprising

GX₃LXEVALG (SEQ ID NO: 20),

GX₂SX₄GX₃PX_aLXGX₂V (SEQ ID NO: 21), and

E(Y/F)X₂YX₃QX₄YLL (SEQ ID NO: 22)

in which a is 7 to 9 and

X is any amino acid, wherein

E(Y/F)X₂YX₃QX₄YLL (SEQ ID NO: 22

is closest to the C terminus.